

Re-run

RAW SEQUENCE LISTING

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Application Serial Number: 10/019,368
Source: PCT
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/019,368

DATE: 08/05/2005

TIME: 10:59:47

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\08042005\J019368.raw

4 <110> APPLICANT: Dean, Nicholas M.
5 ISIS PHARMACEUTICALS, INC.
7 <120> TITLE OF INVENTION: Antisense Oligonucleotide Modulation of Human Protein
8 Kinase C-delta Expression
10 <130> FILE REFERENCE: ISPH-0458
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/019,368
C--> 12 <141> CURRENT FILING DATE: 2001-11-13
12 <150> PRIOR APPLICATION NUMBER: US 09/313,930
13 <151> PRIOR FILING DATE: 1999-05-18
16 <160> NUMBER OF SEQ ID NOS: 20
18 <170> SOFTWARE: PatentIn Ver. 2.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 2104
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (59)..(2089)
29 <300> PUBLICATION INFORMATION:
30 <301> AUTHORS: Aris, J. P.
31 Basta, P. V.
32 Holmes, W. D.
33 Ballas, L. M.
34 Moomaw, C.
35 Rankl, N. B.
36 Blöbel, G.
37 Loomis, C. R.
38 Burns, D. J.
39 <302> TITLE: Molecular and biochemical characterization of a
40 recombinant human PKC-delta family member
41 <303> JOURNAL: Biochim. Biophys. Acta
42 <304> VOLUME: 1174
43 <305> ISSUE: 2
44 <306> PAGES: 171-181
45 <307> DATE: 1993-08-19
46 <308> DATABASE ACCESSION NO: L07860
47 <309> DATABASE ENTRY DATE: 1993-11-02
49 <400> SEQUENCE: 1
50 tgcgcgcgcg acccttggcg cctgcccctg caacggggagc cccactgcag gcccacc 58
52 atg gcg cgc ttc ctg cgc atc gcc ttc aac tcc tat gag ctg ggc tcc 106
53 Met Ala Pro Phe Leu Arg Ile Ala Phe Asn Ser Tyr Glu Leu Gly Ser
54 1 5 10 15
56 ctg cag gcc gag gac gag gcg aac cag ccc ttc tgt gcc gtg aag atg 154

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57  Leu Gln Ala Glu Asp Glu Ala Asn Gln Pro Phe Cys Ala Val Lys Met
58              20              25              30
60  aag gag gcg ctg agc aca gag cgt ggg aaa aca ctg gtg cag aag aag 202
61  Lys Glu Ala Leu Ser Thr Glu Arg Gly Lys Thr Leu Val Gln Lys Lys
62              35              40              45
64  ccg acc atg tat cct gag tgg aag tcg acg ttc gat gcc cac atc tat 250
65  Pro Thr Met Tyr Pro Glu Trp Lys Ser Thr Phe Asp Ala His Ile Tyr
66              50              55              60
68  gag ggg cgc gtc atc cag att gtg cta atg cgg gca gca gag gag cca 298
69  Glu Gly Arg Val Ile Gln Ile Val Leu Met Arg Ala Ala Glu Glu Pro
70              65              70              75              80
72  gtg tct gag gtg acc gtg ggt gtg tcg gtg ctg gcc gag cgc tgc aag 346
73  Val Ser Glu Val Thr Val Gly Val Ser Val Leu Ala Glu Arg Cys Lys
74              85              90              95
76  aag aac aat ggc aag gct gag ttc tgg ctg gac ctg cag cct cag gcc 394
77  Lys Asn Asn Gly Lys Ala Glu Phe Trp Leu Asp Leu Gln Pro Gln Ala
78              100              105              110
80  aag gtg ttg atg tct gtt cag tat ttc ctg gag gac gtg gat tgc aaa 442
81  Lys Val Leu Met Ser Val Gln Tyr Phe Leu Glu Asp Val Asp Cys Lys
82              115              120              125
84  caa tct atg cgc agt gag gac gag gcc aag ttc cca acg atg aac cgc 490
85  Gln Ser Met Arg Ser Glu Asp Glu Ala Lys Phe Pro Thr Met Asn Arg
86              130              135              140
88  cgc gga gcc atc aaa cag gcc aaa atc cac tac atc aag aac cat gag 538
89  Arg Gly Ala Ile Lys Gln Ala Lys Ile His Tyr Ile Lys Asn His Glu
90              145              150              155              160
92  ttt atc gcc acc ttc ttt ggg caa ccc acc ttc tgt tct gtg tgc aaa 586
93  Phe Ile Ala Thr Phe Phe Gly Gln Pro Thr Phe Cys Ser Val Cys Lys
94              165              170              175
96  gac ttt gtc tgg ggc ctg aac aag caa ggc tac aaa tgc agg caa tgt 634
97  Asp Phe Val Trp Gly Leu Asn Lys Gln Gly Tyr Lys Cys Arg Gln Cys
98              180              185              190
100  aac gct gcc atc cac aag aaa tgc atc gac aag atc atc gcc aga tgc 682
101  Asn Ala Ala Ile His Lys Lys Cys Ile Asp Lys Ile Ile Gly Arg Cys
102              195              200              205
104  act ggc acc gcg gcc aac agc cgg gac act ata ttc cag aaa gaa cgc 730
105  Thr Gly Thr Ala Ala Asn Ser Arg Asp Thr Ile Phe Gln Lys Glu Arg
106              210              215              220
108  ttc aac atc gac atg ccg cac cgc ttc aag gtt cac aac tac atg agc 778
109  Phe Asn Ile Asp Met Pro His Arg Phe Lys Val His Asn Tyr Met Ser
110              225              230              235              240
112  ccc acc ttc tgt gac cac tgc ggc agc ctg ctg tgg gga ctg gtg aag 826
113  Pro Thr Phe Cys Asp His Cys Gly Ser Leu Leu Trp Gly Leu Val Lys
114              245              250              255
116  cag gga tta aag tgt gaa gac tgc ggc atg aat gtg cac cat aaa tgc 874
117  Gln Gly Leu Lys Cys Glu Asp Cys Gly Met Asn Val His His Lys Cys
118              260              265              270
120  cgg gag aag gtg gcc aac ctg tgc ggc atc aac cag aag ctt ttg gct 922
121  Arg Glu Lys Val Ala Asn Leu Cys Gly Ile Asn Gln Lys Leu Leu Ala

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122          275          280          285
124   gag gcc ttg aac caa gtc acc cag aga gcc tcc cgg aga tca gac tca   970
125   Glu Ala Leu Asn Gln Val Thr Gln Arg Ala Ser Arg Arg Ser Asp Ser
126          290          295          300
128   gcc tcc tca gag cct gtt ggg ata tat cag ggt ttc gag aag aag acc   1018
129   Ala Ser Ser Glu Pro Val Gly Ile Tyr Gln Gly Phe Glu Lys Lys Thr
130          305          310          315          320
132   gga gtt gct ggg gag gac atg caa gac aac agt ggg acc tac ggc aag   1066
133   Gly Val Ala Gly Glu Asp Met Gln Asp Asn Ser Gly Thr Tyr Gly Lys
134          325          330          335
136   atc tgg gag ggc agc agc aag tgc aac atc aac aac ttc atc ttc cac   1114
137   Ile Trp Glu Gly Ser Ser Lys Cys Asn Ile Asn Asn Phe Ile Phe His
138          340          345          350
140   aag gtc ctg ggc aaa ggc agc ttc ggg aag gtg ctg ctt gga gag ctg   1162
141   Lys Val Leu Gly Lys Gly Ser Phe Gly Lys Val Leu Leu Gly Glu Leu
142          355          360          365
144   aag ggc aga gga gag tac tct gcc atc aag gcc ctc aag aag gat gtg   1210
145   Lys Gly Arg Gly Glu Tyr Ser Ala Ile Lys Ala Leu Lys Lys Asp Val
146          370          375          380
148   gtc ctg atc gac gac gac gtg gag tgc acc atg gtt gag aag cgg gtg   1258
149   Val Leu Ile Asp Asp Asp Val Glu Cys Thr Met Val Glu Lys Arg Val
150          385          390          395          400
152   ctg aca ctt gcc gca gag aat ccc ttt ctc acc cac ctc atc tgc acc   1306
153   Leu Thr Leu Ala Ala Glu Asn Pro Phe Leu Thr His Leu Ile Cys Thr
154          405          410          415
156   ttc cag acc aag gac cac ctg ttc ttt gtg atg gag ttc ctc aac ggg   1354
157   Phe Gln Thr Lys Asp His Leu Phe Phe Val Met Glu Phe Leu Asn Gly
158          420          425          430
160   ggg gac ctg atg tac cac atc cag gac aaa ggc cgc ttt gaa ctc tac   1402
161   Gly Asp Leu Met Tyr His Ile Gln Asp Lys Gly Arg Phe Glu Leu Tyr
162          435          440          445
164   cgt gcc acg ttt tat gcc gct gag ata atg tgt gga ctg cag ttt cta   1450
165   Arg Ala Thr Phe Tyr Ala Ala Glu Ile Met Cys Gly Leu Gln Phe Leu
166          450          455          460
168   cac agc aag ggc atc att tac agg gac ctc aaa ctg gac aat gtg ctg   1498
169   His Ser Lys Gly Ile Ile Tyr Arg Asp Leu Lys Leu Asp Asn Val Leu
170          465          470          475          480
172   ttg gac cgg gat ggc cac atc aag att gcc gac ttt ggg atg tgc aaa   1546
173   Leu Asp Arg Asp Gly His Ile Lys Ile Ala Asp Phe Gly Met Cys Lys
174          485          490          495
176   gag aac ata ttc ggg gag agc cgg gcc agc acc ttc tgc ggc acc cct   1594
177   Glu Asn Ile Phe Gly Glu Ser Arg Ala Ser Thr Phe Cys Gly Thr Pro
178          500          505          510
180   gac tat atc gcc cct gag atc cta cag ggc ctg aag tac aca ttc tct   1642
181   Asp Tyr Ile Ala Pro Glu Ile Leu Gln Gly Leu Lys Tyr Thr Phe Ser
182          515          520          525
184   gtg gac tgg tgg tct ttc ggg gtc ctt ctg tac gag atg ctc att ggc   1690
185   Val Asp Trp Trp Ser Phe Gly Val Leu Leu Tyr Glu Met Leu Ile Gly
186          530          535          540

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188   cag tcc ccc ttc cat ggt gat gat gag gat gaa ctc ttc gag tcc atc   1738
189   Gln Ser Pro Phe His Gly Asp Asp Glu Asp Glu Leu Phe Glu Ser Ile
190   545                               550                               555                               560
192   cgt gtg gac acg cca cat tat ccc cgc tgg atc acc aag gag tcc aag   1786
193   Arg Val Asp Thr Pro His Tyr Pro Arg Trp Ile Thr Lys Glu Ser Lys
194   565                               570                               575
196   gac atc ctg gag aag ctc ttt gaa agg gaa cca acc aag agg ctg gga   1834
197   Asp Ile Leu Glu Lys Leu Phe Glu Arg Glu Pro Thr Lys Arg Leu Gly
198   580                               585                               590
200   atg acg gga aac atc aaa atc cac ccc ttc ttc aag acc ata aac tgg   1882
201   Met Thr Gly Asn Ile Lys Ile His Pro Phe Phe Lys Thr Ile Asn Trp
202   595                               600                               605
204   act ctg ctg gaa aag cgg agg ttg gag cca ccc ttc agg ccc aaa gtg   1930
205   Thr Leu Leu Glu Lys Arg Arg Leu Glu Pro Pro Phe Arg Pro Lys Val
206   610                               615                               620
208   aag tca ccc aga gac tac agt aac ttt gac cag gag ttc ctg aac gag   1978
209   Lys Ser Pro Arg Asp Tyr Ser Asn Phe Asp Gln Glu Phe Leu Asn Glu
210   625                               630                               635                               640
212   aag gcg cgc ctc tcc tac agc gac aag aac ctc atc gac tcc atg gac   2026
213   Lys Ala Arg Leu Ser Tyr Ser Asp Lys Asn Leu Ile Asp Ser Met Asp
214   645                               650                               655
216   cag tct gca ttc gct ggc ttc tcc ttt gtg aac ccc aaa ttc gag cac   2074
217   Gln Ser Ala Phe Ala Gly Phe Ser Phe Val Asn Pro Lys Phe Glu His
218   660                               665                               670
220   ctc ctg gaa gat tga ggttcctgga cagat   2104
221   Leu Leu Glu Asp
222   675
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227 <212> TYPE: PRT
228 <213> ORGANISM: Homo sapiens
230 <400> SEQUENCE: 2
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235   20                               25                               30
237   Lys Glu Ala Leu Ser Thr Glu Arg Gly Lys Thr Leu Val Gln Lys Lys
238   35                               40                               45
240   Pro Thr Met Tyr Pro Glu Trp Lys Ser Thr Phe Asp Ala His Ile Tyr
241   50                               55                               60
243   Glu Gly Arg Val Ile Gln Ile Val Leu Met Arg Ala Ala Glu Glu Pro
244   65                               70                               75                               80
246   Val Ser Glu Val Thr Val Gly Val Ser Val Leu Ala Glu Arg Cys Lys
247   85                               90                               95
249   Lys Asn Asn Gly Lys Ala Glu Phe Trp Leu Asp Leu Gln Pro Gln Ala
250   100                              105                              110
252   Lys Val Leu Met Ser Val Gln Tyr Phe Leu Glu Asp Val Asp Cys Lys
253   115                              120                              125
255   Gln Ser Met Arg Ser Glu Asp Glu Ala Lys Phe Pro Thr Met Asn Arg

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256      130      135      140
258 Arg Gly Ala Ile Lys Gln Ala Lys Ile His Tyr Ile Lys Asn His Glu
259 145      150      155      160
261 Phe Ile Ala Thr Phe Phe Gly Gln Pro Thr Phe Cys Ser Val Cys Lys
262      165      170      175
264 Asp Phe Val Trp Gly Leu Asn Lys Gln Gly Tyr Lys Cys Arg Gln Cys
265      180      185      190
267 Asn Ala Ala Ile His Lys Lys Cys Ile Asp Lys Ile Ile Gly Arg Cys
268      195      200      205
270 Thr Gly Thr Ala Ala Asn Ser Arg Asp Thr Ile Phe Gln Lys Glu Arg
271      210      215      220
273 Phe Asn Ile Asp Met Pro His Arg Phe Lys Val His Asn Tyr Met Ser
274 225      230      235      240
276 Pro Thr Phe Cys Asp His Cys Gly Ser Leu Leu Trp Gly Leu Val Lys
277      245      250      255
279 Gln Gly Leu Lys Cys Glu Asp Cys Gly Met Asn Val His His Lys Cys
280      260      265      270
282 Arg Glu Lys Val Ala Asn Leu Cys Gly Ile Asn Gln Lys Leu Leu Ala
283      275      280      285
285 Glu Ala Leu Asn Gln Val Thr Gln Arg Ala Ser Arg Arg Ser Asp Ser
286      290      295      300
288 Ala Ser Ser Glu Pro Val Gly Ile Tyr Gln Gly Phe Glu Lys Lys Thr
289 305      310      315      320
291 Gly Val Ala Gly Glu Asp Met Gln Asp Asn Ser Gly Thr Tyr Gly Lys
292      325      330      335
294 Ile Trp Glu Gly Ser Ser Lys Cys Asn Ile Asn Asn Phe Ile Phe His
295      340      345      350
297 Lys Val Leu Gly Lys Gly Ser Phe Gly Lys Val Leu Leu Gly Glu Leu
298      355      360      365
300 Lys Gly Arg Gly Glu Tyr Ser Ala Ile Lys Ala Leu Lys Lys Asp Val
301      370      375      380
303 Val Leu Ile Asp Asp Asp Val Glu Cys Thr Met Val Glu Lys Arg Val
304      385      390      395      400
306 Leu Thr Leu Ala Ala Glu Asn Pro Phe Leu Thr His Leu Ile Cys Thr
307      405      410      415
309 Phe Gln Thr Lys Asp His Leu Phe Phe Val Met Glu Phe Leu Asn Gly
310      420      425      430
312 Gly Asp Leu Met Tyr His Ile Gln Asp Lys Gly Arg Phe Glu Leu Tyr
313      435      440      445
315 Arg Ala Thr Phe Tyr Ala Ala Glu Ile Met Cys Gly Leu Gln Phe Leu
316      450      455      460
318 His Ser Lys Gly Ile Ile Tyr Arg Asp Leu Lys Leu Asp Asn Val Leu
319      465      470      475      480
321 Leu Asp Arg Asp Gly His Ile Lys Ile Ala Asp Phe Gly Met Cys Lys
322      485      490      495
324 Glu Asn Ile Phe Gly Glu Ser Arg Ala Ser Thr Phe Cys Gly Thr Pro
325      500      505      510
327 Asp Tyr Ile Ala Pro Glu Ile Leu Gln Gly Leu Lys Tyr Thr Phe Ser
328      515      520      525

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VERIFICATION SUMMARY

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Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\08042005\J019368.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date